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RAW SEQUENCE LISTING

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Application Serial Number: 10/719,692

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DATE: 03/18/2005

PATENT APPLICATION: US/10/719,692

TIME: 08:55:32

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1 <110> APPLICANT: An, Songzhu
2      Chen, Jin-Long
3      Tian, Hui
4      Zhong, Wendy Wen
5      Tularik Inc.
6 <120> TITLE OF INVENTION: Receptor Ligands and Methods of Modulating Receptors
7 <130> FILE REFERENCE: 018781-009530US
8 <140> CURRENT APPLICATION NUMBER: US/10/719,692
9 <141> CURRENT FILING DATE: 2003-11-21
10 <150> PRIOR APPLICATION NUMBER: US 60/421,142
11 <151> PRIOR FILING DATE: 2002-11-25
12 <150> PRIOR APPLICATION NUMBER: US 60/444,153
13 <151> PRIOR FILING DATE: 2003-01-30
14 <160> NUMBER OF SEQ ID NOS: 9
15 <170> SOFTWARE: PatentIn Ver. 2.1
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18 <211> LENGTH: 1164
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
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22 <223> OTHER INFORMATION: human G-protein coupled receptor TGR4a (HM74)
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27      tccagccgga ttttctgtt caacctggca gtagctgact ttctactgat catctgcctg 240
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29      cggtcggtgc tcttcatgtt tgccatgaac cgccagggca gcatcatctt cctcacggtg 360
30      gtggcggtag acaggtatct ccgggtggtc catccccacc acgcctgaa caagatctcc 420
31      aattggacag cagccatcat ctcttgccct ctgtggggca tcaactgttg cctaacagtc 480
32      cacctcctga agaagaagtt gctgatccag aatggccctg caaatgtgtg catcagcttc 540
33      agcatctgcc ataccttccg gtggcacgaa gctatgttcc tcttgaggtt cctcctgccc 600
34      ctgggcatca tctgttctg ctacgccaga attatctgga gcctgcggca gagacaaatg 660
35      gaccggcatg ccaagatcaa gagagccatc accttcatca tgggtggtggc catcgtcttt 720
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38      agcttcacct acatgaacag catgctggac ccggtggtgt actacttctc cagcccatcc 900
39      tttcccaact tcttctccac tttgatcaac cgctgcctcc agaggaagat gacaggtgag 960
40      ccagataata accgcagcac gacgctcgag ctacagggg accccaacaa aaccagaggc 1020
41      gctccagagg cgtaaatggc caactccggt gagccatgga gccctcttta tctgggcca 1080
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54 Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro
55 20 25 30
56 Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
57 35 40 45
58 Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
59 50 55 60
60 Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
61 65 70 75 80
62 Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Asn Phe Gly
63 85 90 95
64 Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln
65 100 105 110
66 Gly Ser Ile Ile Phe Leu Thr Val Ala Val Asp Arg Tyr Phe Arg
67 115 120 125
68 Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala
69 130 135 140
70 Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val
71 145 150 155 160
72 His Leu Leu Lys Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val
73 165 170 175
74 Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met
75 180 185 190
76 Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser
77 195 200 205
78 Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala
79 210 215 220
80 Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe
81 225 230 235 240
82 Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp
83 245 250 255
84 Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val
85 260 265 270
86 Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
87 275 280 285
88 Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe
89 290 295 300
90 Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu
91 305 310 315 320
92 Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn
93 325 330 335
94 Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro

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96      Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys
97          355          360          365
98      Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys
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100      Cys Ile Glu
101      385
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105 <212> TYPE: DNA
106 <213> ORGANISM: Homo sapiens
107 <220> FEATURE:
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112      gggcttcttg gcaatggcct tgccctgttg attttctgtt tccacctcaa gtcttgaaa 180
113      tccagccgga ttttctgtt caacctggca gtggctgact ttctactgat catctgcctg 240
114      cccttctga tggacaacta tgtgaggcgt tgggactgga agtttgaggga catcccttgc 300
115      cggctgatgc tcttcattgt ggctatgaac cgccagggca gcatcatctt cctcacggtg 360
116      gtggcggtag acaggtattt ccgggtggtc catccccacc acgccctgaa caagatctcc 420
117      aatcggaacag cagccatcat ctcttgctt ctgtggggca tcaactattg cctgacagtc 480
118      cactcctga agaagaagat gccgatccag aatggcggtg caaatttgtg cagcagcttc 540
119      agcatctgcc ataccttcca gtggcacgaa gccatgttcc tcttgaggtt ctctctgcc 600
120      ctgggcatca tctgttctg ctacgccaga attatctgga gcctgcggca gagacaaatg 660
121      gaccggcatg ccaagatcaa gagagccatc accttcatca tgggtggtggc catcgtcttt 720
122      gtcactctgt tcttcccgag cgtggttgtg cggatccgca tcttctggct cctgcacact 780
123      tcgggcacgc agaattgtga agtgaccgc tcggtggacc tggcgttctt tatcactctc 840
124      agcttcacct acatgaacag catgctggac cccgtggtgt actacttctc cagcccatcc 900
125      tttcccaact tcttctccac tttgatcaac cgctgcctcc agaggaagat gacaggtgag 960
126      ccagataata accgcagcac gagcgctcag ctacagggg accccaacaa aaccagaggc 1020
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128      acctctctt aa 1092
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131 <211> LENGTH: 363
132 <212> TYPE: PRT
133 <213> ORGANISM: Homo sapiens
134 <220> FEATURE:
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136 <400> SEQUENCE: 4
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140          20          25          30
141      Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
142          35          40          45
143      Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
144          50          55          60
145      Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu

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147  Pro Phe Leu Met Asp Asn Tyr Val Arg Arg Trp Asp Trp Lys Phe Gly
148      85      90      95
149  Asp Ile Pro Cys Arg Leu Met Leu Phe Met Leu Ala Met Asn Arg Gln
150      100      105      110
151  Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg
152      115      120      125
153  Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Arg Thr Ala
154      130      135      140
155  Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Ile Gly Leu Thr Val
156      145      150      155      160
157  His Leu Leu Lys Lys Lys Met Pro Ile Gln Asn Gly Gly Ala Asn Leu
158      165      170      175
159  Cys Ser Ser Phe Ser Ile Cys His Thr Phe Gln Trp His Glu Ala Met
160      180      185      190
161  Phe Leu Leu Glu Phe Phe Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser
162      195      200      205
163  Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala
164      210      215      220
165  Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe
166      225      230      235      240
167  Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp
168      245      250      255
169  Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val
170      260      265      270
171  Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
172      275      280      285
173  Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe
174      290      295      300
175  Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu
176      305      310      315      320
177  Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn
178      325      330      335
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182      355      360
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186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
188 <220> FEATURE:
189 <223> OTHER INFORMATION: human G-protein coupled receptor TGR183
190 <400> SEQUENCE: 5
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192  ctgctcattg tggcctttgt gctgggcgca ctaggcaatg gggtcgccct gtgtgggttc 120
193  tgcttcacac tgaagacctg gaagcccagc actgtttacc ttttcaattt ggccgtggct 180
194  gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac 240
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196 gggagcatcg tgttccttac ggtggtggct gcggacaggt atttcaaagt ggtccacccc 360
197 caccacgagg tgaacactat ctccaccggg gtggcggctg gcacgtctcg caccctgtgg 420
198 gccctgggtca tcttggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag 480
199 acggccgtct cctgtgagag cttcatcatg gactcggcca atggctggca tgacatcatg 540
200 ttccagctgg agttctttat gccctcggc atcatcttat tttgtcctt caagattgtt 600
201 tggagcctga ggcgaggga gcagctggcc agacaggctc ggatgaagaa ggcgaccgg 660
202 ttcatcatgg tggaggcaat tgtgttcac acatgctacc tgcccagcgt gctgctaga 720
203 ctctatttcc tctggacggt gccctcgagt gcctgcgac cctctgtcca tggggccctg 780
204 cacataaccc tcagcttcac ctacatgaac agcatgctgg atcccctggg gtattatttt 840
205 tcaagcccct cttttccaa attctacaac aagctcaaaa tctgcagtct gaaacccaag 900
206 cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc 960
207 aggagtgtga tcagtgtggc aaatagtttc caaagccagt ctgatgggca atgggatccc 1020
208 cacattgttg agtggcactg a                                     1041
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211 <211> LENGTH: 346
212 <212> TYPE: PRT
213 <213> ORGANISM: Homo sapiens
214 <220> FEATURE:
215 <223> OTHER INFORMATION: human G-protein coupled receptor TGR183
216 <400> SEQUENCE: 6
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220 20 25 30
221 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
222 35 40 45
223 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
224 50 55 60
225 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
226 65 70 75 80
227 Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
228 85 90 95
229 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
230 100 105 110
231 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
232 115 120 125
233 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
234 130 135 140
235 Leu Gly Thr Val Tyr Leu Leu Glu Asn His Leu Cys Val Gln Glu
236 145 150 155 160
237 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
238 165 170 175
239 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
240 180 185 190
241 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
242 195 200 205
243 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
244 210 215 220
245 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg

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